Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *09/545, 1998*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
.   prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                  ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                        each n or Xaa can only represent a single residue. Please present the maximum number of each
                        residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                    the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                    Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         This sequence is intentionally skipped

                         Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
                         <400> sequence id number
                         000

9_✓_Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                         In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                       is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                      "Unknown." Please explain source of genetic material in <220> to <223> section.
                      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____✓_PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                       listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

1643

```
        RAW SEQUENCE LISTING              DATE: 06/27/2001
        PATENT APPLICATION:  US/09/545,199B      TIME: 12:40:15
```

Does Not Comply
Corrected Diskette Needed

```
        Input Set : C:\Crf3\Datahold\09545199
        Output Set: N:\CRF3\06262001\I545199B.raw
```

```
C-->  2 <140> CURRENT APPLICATION NUMBER: US/09/545,199B
C-->  2 <141> CURRENT FILING DATE: 2000-04-06
W-->  2 <151> PRIOR FILING DATE: 1999-09-10
W-->  0 <110> APPLICANT:
W-->  0 <120> TITLE INVENTION:
W-->  0 <130> FILE REFERENCE:
      4 <150> PRIOR APPLICATION NUMBER: 60/128,689
      5 <151> PRIOR FILING DATE: 1999-04-09
      7 <160> NUMBER OF SEQ ID NOS: 165
      9 <170> SOFTWARE: PatentIn Ver. 2.0
```

These mandatory features are missing from file. Possible Patentin 2.0 "bug". See #12 on the Error Summary Sheet.

ERRORED SEQUENCES

```
   1952 <210> SEQ ID NO: 16
   1953 <211> LENGTH: 2110
   1954 <212> TYPE: PRT
   1955 <213> ORGANISM: Pasteurella multocida
   1957 <400> SEQUENCE: 16
   1958 Met Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn
   1959  1               5                   10                  15
   1961 Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala
   1962             20                  25                  30
   1964 Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
   1965         35                  40                  45
   1967 Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
   1968       50                  55                  60
   1970 Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg
   1971  65                  70                  75                  80
   1973 Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
   1974             85                  90                  95
   1976 Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala
   1977             100                 105                 110
   1979 Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser
   1980         115                 120                 125
   1982 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys
   1983         130                 135                 140
   1985 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
   1986 145                 150                 155                 160
   1988 Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile
   1989             165                 170                 175
   1991 Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser
   1992             180                 185                 190
   1994 Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala
   1995             195                 200                 205
   1997 Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu
   1998         210                 215                 220
```

```
2000 Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
2001 225             230             235                 240
2003 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
2004             245             250             255
2006 Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
2007         260             265             270
2009 Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
2010         275             280             285
2012 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
2013     290             295             300
2015 Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser
2016 305             310             315                 320
2018 Leu Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu
2019             325             330             335
2021 Glu Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met
2022             340             345             350
2024 Pro Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu
2025         355             360             365
2027 Ser Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile
2028     370             375             380
2030 Glu Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp
2031 385             390             395                 400
2033 Asp Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu
2034             405             410             415
2036 Lys Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly
2037         420             425             430
2039 Asn Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp
2040         435             440             445
2042 Glu Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu
2043     450             455             460
2045 Gly Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser
2046 465             470             475                 480
2048 Thr Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys
2049             485             490             495
2051 Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
2052         500             505             510
2054 Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
2055         515             520             525
2057 Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
2058     530             535             540
2060 Lys Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp
2061 545             550             555                 560
2063 Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
2064             565             570             575
2066 Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
2067         580             585             590
2069 Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
2070         595             600             605
2072 Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu
```

```
2073      610                    615           .          620
2075 Asp Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala
2076 625                    630           .       635                640
2078 Glu Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro
2079                    645               650               655
2081 Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn
2082               660               665               670
2084 Gln Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu
2085          675               680               685
2087 Asn Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe
2088     690               695               700
2090 Asp His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His
2091 705                    710 ·              715                   720
2093 Leu Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu
2094               725               730               735
2096 Met Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly
2097               740               745               750
2099 Ala Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val
2100          755               760               765
2102 Trp Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys
2103      770               775               780
2105 Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly
2106 785               790               795                800
2108 Leu Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys
2109               805               810               815
2111 Asp Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu
2112          820               825               830
2114 Ala Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu
2115          835               840               845
2117 Thr Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe
2118      850               855               860
2120 Ala Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr
2121 865                    870               875                880
2123 Glu Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val
2124               885               890               895
2126 Gln Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp
2127          900        ·           905               910
2129 Val Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys
2130      ·   915               920               925
2132 Phe Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu
2133      930               935               940 ·
2135 Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His
2136 945           ·      950               955    ·              960
2138 Thr Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu
2139               965               970          ·     975
2141 His Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys
2142          980               985               990
2144 Ala Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala
2145          995               1000              1005
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RAW SEQUENCE LISTING   DATE: 06/27/2001
PATENT APPLICATION: US/09/545,199B   TIME: 12:40:15

Input Set : C:\Crf3\Datahold\09545199
Output Set: N:\CRF3\06262001\I545199B.raw

```
      2147 Gly Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu
      2148      1010               1015               1020
      2150 Phe Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp
E--> 2151 025               1030               1035               1040
      2153 Tyr Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn
      2154                1045               1050               1055
      2156 His Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys
      2157           1060               1065               1070
      2159 Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
      2160        1075               1080               1085
      2162 His Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp
      2163      1090               1095               1100
      2165 Ile Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu
E--> 2166 105               1110               1115               1120
      2168 Ile Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val
      2169                1125               1130               1135
      2171 Ala Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro
      2172                1140               1145               1150
      2174 Glu Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu
      2175      1155               1160               1165
      2177 Lys Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala
      2178      1170               1175               1180
      2180 Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
E--> 2181 185               1190               1195               1200
      2183 Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
      2184                1205               1210               1215
      2186 Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
      2187           1220               1225               1230
      2189 His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
      2190      1235               1240               1245
      2192 Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
      2193      1250               1255               1260
      2195 Gly Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His
E--> 2196 265               1270               1275               1280
      2198 Glu Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly
      2199           1285               1290               1295
      2201 Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
      2202           1300               1305               1310
      2204 Val Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp
      2205      1315               1320               1325
      2207 Val Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val
      2208      1330               1335               1340
      2210 Ser Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met
E--> 2211 345               1350               1355               1360
      2213 Ser Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu
      2214      1365               1370               1375
      2216 Ser Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys
      2217      1380               1385               1390
      2219 Ala Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser
```

misaligned amino acid numbers. First digit of number must be under the first letter of the amino acid.

Phe
1025

Ile
1105

Pro
1185

Gly
1265

Ser
1345

RAW SEQUENCE LISTING   DATE: 06/27/2001
PATENT APPLICATION: **US/09/545,199B**   TIME: 12:40:15

Input Set : **C:\Crf3\Datahold\09545199**
Output Set: **N:\CRF3\06262001\I545199B.raw**

```
      2220        1395              1400              1405
      2222 Ser Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr
      2223      1410              1415              1420
      2225 Asn Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val
E--> 2226  425               1430              1435              1440
      2228 Asp Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala
      2229              1445              1450              1455
      2231 Thr Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser
      2232            1460              1465              1470
      2234 Lys Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr
      2235         1475              1480              1485
      2237 Gly Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn
      2238         1490              1495              1500
      2240 Asp Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala
E--> 2241  505               1510              1515              1520
      2243 Leu His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val
      2244              1525              1530              1535
      2246 Gly Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg
      2247              1540              1545              1550
      2249 Ala Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly
      2250         1555              1560              1565
      2252 Val Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu
      2253        1570              1575              1580
      2255 Thr Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln
E--> 2256  585               1590              1595              1600
      2258 Phe Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys
      2259              1605              1610              1615
      2261 Asn Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser
      2262         1620              1625              1630
      2264 Thr Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr
      2265         1635              1640              1645
      2267 Arg Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro
      2268         1650              1655              1660
      2270 Ile Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn
E--> 2271  665               1670              1675              1680
      2273 Val Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr
      2274              1685              1690              1695
      2276 Thr Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser
      2277         1700              1705              1710
      2279 Lys Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr
      2280         1715              1720              1725
      2282 Ser Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg
      2283      1730              1735              1740
      2285 Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
E--> 2286  745               1750              1755              1760
      2288 Thr Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp
      2289              1765              1770              1775
      2291 Pro Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp
      2292         1780              1785              1790
```

Same error
See
p. 4

RAW SEQUENCE LISTING   DATE: 06/27/2001
PATENT APPLICATION: US/09/545,199B   TIME: 12:40:15

Input Set : C:\Crf3\Datahold\09545199
Output Set: N:\CRF3\06262001\I545199B.raw

```
        2294 Gly Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr
        2295      1795              1800              1805
        2297 Lys Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn
        2298      1810              1815              1820
        2300 Ala Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser
E-->    2301  825              1830              1835              1840
        2303 Pro Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn
        2304              1845              1850              1855
        2306 Lys Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys
        2307      1860              1865              1870
        2309 Ala Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu
        2310      1875              1880              1885
        2312 Arg Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn
        2313      1890              1895              1900
        2315 Lys Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu
E-->    2316  905              1910              1915              1920
        2318 Phe Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala
        2319              1925              1930              1935
        2321 Ile Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val
        2322              1940              1945              1950
        2324 Val Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala
        2325      1955              1960              1965
        2327 Pro Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp
        2328      1970              1975              1980
        2330 Ala Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg
E-->    2331  985              1990              1995              2000
        2333 Arg Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys
        2334              2005              2010              2015
        2336 Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala
        2337      2020              2025              2030
        2339 His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn
        2340      2035              2040              2045
        2342 Gly Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu
        2343      2050              2055              2060
        2345 Val Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val
E-->    2346  065              2070              2075              2080
        2348 Ile Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu
        2349              2085              2090              2095
        2351 Gly Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
        2352      2100              2105              2110
        3855 <210> SEQ ID NO: 28
        3856 <211> LENGTH: 450
        3857 <212> TYPE: PRT
        3858 <213> ORGANISM: Pasteurella multocida
        3860 <400> SEQUENCE: 28
        3861 Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
        3862   1               5               10              15
        3864 Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
        3865      20              25              30
```

Same ¢ See p. (handwritten)

→ *See next page* (handwritten)

```
       3867 Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
       3868          35               40                   45
       3870 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
       3871          50               55                   60
       3873 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
       3874  65               70                   75                   80
       3876 Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
       3877              85                   90                   95
       3879 Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
       3880          100                  105                  110
E-->   3882 Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
       3883          115                  120                  125
E-->   3885 Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
       3886          130                  135                  140
E-->   3888 Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
       3889 145                  150                  155                  160
       3891 Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
       3892              165                  170                  175
       3894 Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
       3895          180                  185                  190
       3897 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
       3898          195                  200                  205
       3900 Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
       3901          210                  215                  220
       3903 Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
       3904 225                  230                  235                  240
       3906 Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
       3907              245                  250                  255
       3909 Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
       3910          260                  265                  270
       3912 Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln
       3913          275                  280                  285
       3915 Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His
       3916          290                  295                  300
       3918 Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu
       3919 305                  310                  315                  320
       3921 Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
       3922              325                  330                  335
       3924 Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
       3925          340                  345                  350
       3927 Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
       3928          355                  360                  365
       3930 Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
       3931          370                  375                  380
       3933 Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
       3934 385                  390                  395                  400
       3936 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
       3937              405                  410                  415
       3939 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
```

Sequence #28 is missing the mandatory features <220> to <223> to explain the "Xaa's" in the sequence. See the #9 on the Error Summary Sheet.

```
3940              420              425              430
3942 Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
3943         435              440              445
3945 Gln Val
3946    450
5300 <210> SEQ ID NO: 36
5301 <211> LENGTH: 302
5302 <212> TYPE: PRT
5303 <213> ORGANISM: Pasteurella multocida
5305 <400> SEQUENCE: 36
5306 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
5307 1               5              10              15
5309 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
5310             20              25              30
5312 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
5313         35              40              45
5315 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
5316     50              55              60
5318 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
5319 65              70              75              80
5321 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
5322             85              90              95
5324 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
5325             100             105             110
5327 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
5328         115             120             125
5330 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
5331     130             135             140
5333 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
5334 145             150             155             160
5336 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
5337             165             170             175
5339 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
5340             180             185             190
5342 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
5343         195             200             205
5345 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
5346     210             215             220
5348 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
5349 225             230             235             240
5351 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
5352             245             250             255
5354 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
5355         260             265             270
5357 Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
5358     275             280             285
5360 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
5361     290             295             300
5472 <210> SEQ ID NO: 38
```

E--> 5345
E--> 5348
E--> 5354
E--> 5357

[Handwritten annotation:] Missing <220> to <223> features to explain "Xaa's" in the sequence.

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Input Set : C:\Crf3\Datahold\09545199
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```
5473  <211> LENGTH: 166                  missing <220> to <223> features
5474  <212> TYPE: PRT
5475  <213> ORGANISM: Pasteurella multocida    for "Xaa's"
5477  <400> SEQUENCE: 38
5478  Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
5479   1               5                  10                  15
5481  Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
5482          20                  25                  30
E-->  5484  Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
5485        35                  40                  45
5487  Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
5488      50                  55                  60
5490  Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
5491  65                  70                  75                  80
5493  Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
5494              85                  90                  95
E-->  5496  Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
5497          100                 105                 110
5499  Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
5500          115                 120                 125
5502  Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
5503      130                 135                 140
5505  Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
5506  145                 150                 155                 160
5508  Cys Trp Cys Gly Cys Gly
5509                  165               "Xaa" in sequence
11512 <210> SEQ ID NO: 103                          See p. 13
11513 <211> LENGTH: 1643
11514 <212> TYPE: PRT
11515 <213> ORGANISM: Pasteurella multocida
11517 <400> SEQUENCE: 103
11518 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
11519  1               5                  10                  15
11521 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
11522          20                  25                  30
11524 Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
11525          35                  40                  45
11527 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
11528      50                  55                  60
11530 Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
11531  65                  70                  75                  80
11533 Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
11534              85                  90                  95
11536 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
11537              100                 105                 110
11539 Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
11540          115                 120                 125
11542 Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
11543          130                 135                 140
```

```
11545 Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
11546 145               150               155               160
11548 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
11549               165               170               175
11551 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
11552           180               185               190
11554 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
11555           195               200               205
11557 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
11558       210               215               220
11560 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
11561 225               230               235               240
11563 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
11564               245               250               255
11566 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
11567               260               265               270
11569 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
11570           275               280               285
11572 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
11573       290               295               300
11575 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
11576 305               310               315               320
11578 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
11579               325               330               335
11581 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
11582           340               345               350
11584 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
11585       355               360               365
11587 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
11588       370               375               380
11590 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
11591 385               390               395               400
11593 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
11594               405               410               415
11596 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
11597           420               425               430
11599 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
11600       435               440               445
11602 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
11603       450               455               460
11605 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
11606 465               470               475               480
11608 Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
11609               485               490               495
11611 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
11612           500               505               510
11614 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
11615           515               520               525
11617 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
```

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Input Set : C:\Crf3\Datahold\09545199
Output Set: N:\CRF3\06262001\I545199B.raw

```
11618      530                 535                 540
11620 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
11621 545                 550                 555                 560
11623 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
11624                 565                 570                 575
11626 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
11627                 580                 585                 590
11629 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
11630                 595                 600                 605
11632 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
11633      610                 615                 620
11635 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
11636 625                 630                 635                 640
11638 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
11639                 645                 650                 655
11641 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
11642                 660                 665                 670
11644 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
11645                 675                 680                 685
11647 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
11648      690                 695                 700
11650 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
11651 705                 710                 715                 720
11653 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
11654                 725                 730                 735
11656 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
11657                 740                 745                 750
11659 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
11660      755                 760                 765
11662 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
11663      770                 775                 780
11665 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
11666 785                 790                 795                 800
11668 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
11669                 805                 810                 815
11671 Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
11672                 820                 825                 830
11674 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
11675                 835                 840                 845
11677 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
11678      850                 855                 860
11680 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
11681 865                 870                 875                 880
11683 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
11684                 885                 890                 895
11686 Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
11687                 900                 905                 910
11689 Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
11690                 915                 920                 925
```

```
11692 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
11693     930                 935                 940
11695 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
11696 945                 950                 955                 960
11698 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
11699                 965                 970                 975
11701 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
11702                 980                 985                 990
11704 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
11705                 995                 1000                1005
11707 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
11708     1010                1015                1020
11710 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
11711 1025                1030                1035                1040
11713 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
11714                 1045                1050                1055
11716 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
11717             1060                1065                1070
11719 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
11720         1075                1080                1085
11722 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
11723     1090                1095                1100
11725 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
11726 1105                1110                1115                1120
11728 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
11729                 1125                1130                1135
11731 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
11732             1140                1145                1150
11734 Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
11735         1155                1160                1165
11737 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
11738     1170                1175                1180
11740 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
11741 1185                1190                1195                1200
11743 Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
11744             1205                1210                1215
11746 Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
11747             1220                1225                1230
11749 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
11750         1235                1240                1245
11752 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
11753     1250                1255                1260
11755 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
11756 1265                1270                1275                1280
11758 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
11759                 1285                1290                1295
11761 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
11762             1300                1305                1310
11764 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
```

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Input Set : C:\Crf3\Datahold\09545199
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```
11765        1315              1320              1325
11767 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
11768     1330              1335              1340
11770 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
11771 1345             1350              1355              1360
11773 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
11774             1365              1370              1375
11776 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
11777         1380              1385              1390
11779 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
11780        1395              1400              1405
11782 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
11783    1410              1415              1420
11785 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
11786 1425             1430              1435              1440
11788 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
11789             1445              1450              1455
11791 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
11792        1460              1465              1470
11794 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
11795        1475              1480              1485
11797 Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
11798    1490              1495              1500
11800 Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
11801 1505             1510              1515              1520
11803 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
11804             1525              1530              1535
11806 Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
11807        1540              1545              1550
11809 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
11810    1555              1560              1565
11812 Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
11813    1570              1575              1580
11815 Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
11816 1585             1590              1595              1600
11818 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
11819        1605              1610              1615
E--> 11821 Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
11822        1620              1625              1630
11824 Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
11825        1635              1640
```

Xaa in sequence. needs <220> to <223> features. (handwritten annotation)

<210> SEQ ID NO 1
<211> LENGTH: 1112
<212> TYPE: DNA
<213> ORGANISM: Pasteurella multocida
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (210)..(1001)
<223> OTHER INFORMATION: atpB
<400> SEQUENCE: 1

Missing mandatory <220> to <223> features to explain the "n" at position 1104 in the sequence.

```
gtcaacaaca ttttatggtg gagaggccgt taaatttata tccacaattt ttttgattgt  60
acttgctttt aaactgttca attcaatgca ttttattgca tttttttgttg gatattttat 120
aacaatagtt ttaaacaata ttcttccatt ttttataagt aagtacttaa atataaagca 180
ttttcataaa tatcaataaa ggattagtt  atg gca gca gag ctt aca aca gcg  233
                                 Met Ala Ala Glu Leu Thr Thr Ala
                                  1               5

gga tat att ggg cac cat tta gca ttc ttg aaa aca ggg gat tct ttc  281
Gly Tyr Ile Gly His His Leu Ala Phe Leu Lys Thr Gly Asp Ser Phe
         10                  15                  20

tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca  329
Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala
 25                  30                  35                  40

att ttt ctt ttt gtt ttt tca aaa gtt gca aaa aaa gca acg ccg ggt  377
Ile Phe Leu Phe Val Phe Ser Lys Val Ala Lys Lys Ala Thr Pro Gly
                 45                  50                  55

gtg cct agc aag atg caa tgt ttt gtt gag ata atg gtt gat tgg att  425
Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile
                 60                  65                  70

gat ggg atc gta aaa gaa aat ttc cat ggt cct cgt cat gct gtt gga  473
Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly
         75                  80                  85

cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc  521
Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile
         90                  95                 100

gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt  569
Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly
105                 110                 115                 120

att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta  617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu
                125                 130                 135

ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa  665
Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys
                140                 145                 150

tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt  713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe
                155                 160                 165

aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca  761
Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr
         170                 175                 180

tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg  809
Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met
185                 190                 195                 200

tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca  857
Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala
                205                 210                 215

aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg  905
Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp
                220                 225                 230
```

```
gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg   953
Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met
        235                 240                 245
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac   1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His
        250                 255                 260
taatttttta taaacaaaac cagaccttgg gtctaaattt caatcttatg gagaacatta   1061
tggaacactg taattactac aacaatcatc gcatctgnaa t(n)tcttgc t               1112
```

FY. I.
F.
→

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Note: see verification summary on pages 16 and 17 of this listing to see which sequences need "n" or "Xaa" explainations

DATE: 06/27/2001
PATENT APPLICATION: **US/09/545,199B**   TIME: 12:40:17

        Input Set : **C:\Crf3\Datahold\09545199**
        Output Set: **N:\CRF3\06262001\I545199B.raw**

L:2 M:270 C: Current Application Number differs, Replaced Current Application No
L:2 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP NO
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:2151 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2181 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2196 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2241 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2256 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2286 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2316 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2331 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:2346 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:3766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3882 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:3885 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28 /
L:3888 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:5261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5345 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:5348 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36 /
L:5354 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:5357 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:5385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37

VERIFICATION SUMMARY   DATE: 06/27/2001
PATENT APPLICATION: **US/09/545,199B**   TIME: 12:40:17

Input Set : **C:\Crf3\Datahold\09545199**
Output Set: **N:\CRF3\06262001\I545199B.raw**

```
L:5484 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
L:5496 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
L:5609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:6532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:9085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:10782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90
L:10782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
L:10782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90
L:10784 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90
L:10784 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
L:10784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90
L:11503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:11504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:11821 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103
```